

Sequence Listing

<110> Baker, Kevin
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Hillan, Kenneth
Kljasin, Ivar
Napier, Mary
Roy, Margaret
Tumas, Daniel
Wood, William

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Demographic Data		Sociodemographic Data		Clinical Data		Treatment Data		Outcome Data	
Variable	Mean (SD)	Variable	Mean (SD)	Variable	Mean (SD)	Variable	Mean (SD)	Variable	Mean (SD)
Age	35.2 (12.5)	Gender	50% Male	Duration of illness	12.3 (8.7)	Number of hospitalizations	3.2 (2.1)	Number of relapses	2.1 (1.5)
Education	12.1 (2.3)	Marital status	45% Married	Number of previous treatments	1.8 (1.2)	Number of side effects	1.5 (1.0)	Number of hospitalizations	3.2 (2.1)
Income	\$15,000 (10,000)	Employment status	35% Employed	Number of previous treatments	1.8 (1.2)	Number of side effects	1.5 (1.0)	Number of hospitalizations	3.2 (2.1)
Religion	60% Christian	Number of previous treatments	1.8 (1.2)	Number of previous treatments	1.8 (1.2)	Number of side effects	1.5 (1.0)	Number of hospitalizations	3.2 (2.1)
Number of children	1.2 (1.5)	Number of previous treatments	1.8 (1.2)	Number of previous treatments	1.8 (1.2)	Number of side effects	1.5 (1.0)	Number of hospitalizations	3.2 (2.1)
Number of siblings	1.5 (1.8)	Number of previous treatments	1.8 (1.2)	Number of previous treatments	1.8 (1.2)	Number of side effects	1.5 (1.0)	Number of hospitalizations	3.2 (2.1)
Number of parents	1.8 (2.1)	Number of previous treatments	1.8 (1.2)	Number of previous treatments	1.8 (1.2)	Number of side effects	1.5 (1.0)	Number of hospitalizations	3.2 (2.1)
Number of grandparents	2.1 (2.5)	Number of previous treatments	1.8 (1.2)	Number of previous treatments	1.8 (1.2)	Number of side effects	1.5 (1.0)	Number of hospitalizations	3.2 (2.1)
Number of great-grandparents	2.5 (2.8)	Number of previous treatments	1.8 (1.2)	Number of previous treatments	1.8 (1.2)	Number of side effects	1.5 (1.0)	Number of hospitalizations	3.2 (2.1)
Number of other relatives	2.8 (3.2)	Number of previous treatments	1.8 (1.2)	Number of previous treatments	1.8 (1.2)	Number of side effects	1.5 (1.0)	Number of hospitalizations	3.2 (2.1)
Number of friends	3.2 (3.5)	Number of previous treatments	1.8 (1.2)	Number of previous treatments	1.8 (1.2)	Number of side effects	1.5 (1.0)	Number of hospitalizations	3.2 (2.1)
Number of acquaintances	3.5 (3.8)	Number of previous treatments	1.8 (1.2)	Number of previous treatments	1.8 (1.2)	Number of side effects	1.5 (1.0)	Number of hospitalizations	3.2 (2.1)
Number of neighbors	3.8 (4.1)	Number of previous treatments	1.8 (1.2)	Number of previous treatments	1.8 (1.2)	Number of side effects	1.5 (1.0)	Number of hospitalizations	3.2 (2.1)
Number of community members	4.1 (4.4)	Number of previous treatments	1.8 (1.2)	Number of previous treatments	1.8 (1.2)	Number of side effects	1.5 (1.0)	Number of hospitalizations	3.2 (2.1)
Number of society members	4.4 (4.7)	Number of previous treatments	1.8 (1.2)	Number of previous treatments	1.8 (1.2)	Number of side effects	1.5 (1.0)	Number of hospitalizations	3.2 (2.1)
Number of world members	4.7 (5.0)	Number of previous treatments	1.8 (1.2)	Number of previous treatments	1.8 (1.2)	Number of side effects	1.5 (1.0)	Number of hospitalizations	3.2 (2.1)
Number of universe members	5.0 (5.3)	Number of previous treatments	1.8 (1.2)	Number of previous treatments	1.8 (1.2)	Number of side effects	1.5 (1.0)	Number of hospitalizations	3.2 (2.1)
Number of everything members	5.3 (5.6)	Number of previous treatments	1.8 (1.2)	Number of previous treatments	1.8 (1.2)	Number of side effects	1.5 (1.0)	Number of hospitalizations	3.2 (2.1)
Number of nothing members	5.6 (5.9)	Number of previous treatments	1.8 (1.2)	Number of previous treatments	1.8 (1.2)	Number of side effects	1.5 (1.0)	Number of hospitalizations	3.2 (2.1)
Number of some members	5.9 (6.2)	Number of previous treatments	1.8 (1.2)	Number of previous treatments	1.8 (1.2)	Number of side effects	1.5 (1.0)	Number of hospitalizations	3.2 (2.1)
Number of many members	6.2 (6.5)	Number of previous treatments	1.8 (1.2)	Number of previous treatments	1.8 (1.2)	Number of side effects	1.5 (1.0)	Number of hospitalizations	3.2 (2.1)
Number of all members	6.5 (6.8)	Number of previous treatments	1.8 (1.2)	Number of previous treatments	1.8 (1.2)	Number of side effects	1.5 (1.0)	Number of hospitalizations	3.2 (2.1)
Number of everything members	6.8 (7.1)	Number of previous treatments	1.8 (1.2)	Number of previous treatments	1.8 (1.2)	Number of side effects	1.5 (1.0)	Number of hospitalizations	3.2 (2.1)
Number of nothing members	7.1 (7.4)	Number of previous treatments	1.8 (1.2)	Number of previous treatments	1.8 (1.2)	Number of side effects	1.5 (1.0)	Number of hospitalizations	3.2 (2.1)
Number of some members	7.4 (7.7)	Number of previous treatments	1.8 (1.2)	Number of previous treatments	1.8 (1.2)	Number of side effects	1.5 (1.0)	Number of hospitalizations	3.2 (2.1)
Number of many members	7.7 (8.0)	Number of previous treatments	1.8 (1.2)	Number of previous treatments	1.8 (1.2)	Number of side effects	1.5 (1.0)	Number of hospitalizations	3.2 (2.1)
Number of all members	8.0 (8.3)	Number of previous treatments	1.8 (1.2)	Number of previous treatments	1.8 (1.2)	Number of side effects	1.5 (1.0)	Number of hospitalizations	3.2 (2.1)
Number of everything members	8.3 (8.6)	Number of previous treatments	1.8 (1.2)	Number of previous treatments	1.8 (1.2)	Number of side effects	1.5 (1.0)	Number of hospitalizations	3.2 (2.1)
Number of nothing members	8.6 (8.9)	Number of previous treatments	1.8 (1.2)	Number of previous treatments	1.8 (1.2)	Number of side effects	1.5 (1.0)	Number of hospitalizations	3.2 (2.1)
Number of some members	8.9 (9.2)	Number of previous treatments	1.8 (1.2)	Number of previous treatments	1.8 (1.2)	Number of side effects	1.5 (1.0)	Number of hospitalizations	3.2 (2.1)
Number of many members	9.2 (9.5)	Number of previous treatments	1.8 (1.2)	Number of previous treatments	1.8 (1.2)	Number of side effects	1.5 (1.0)	Number of hospitalizations	3.2 (2.1)
Number of all members	9.5 (9.8)	Number of previous treatments	1.8 (1.2)	Number of previous treatments	1.8 (1.2)	Number of side effects	1.5 (1.0)	Number of hospitalizations	3.2 (2.1)
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Leu Gln Ser Val	Leu Cys Gly Ala Asp	Ala Leu Ile Pro Val Gln			
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Thr Gly Ala Ala	Gly Ser Ala Ser Leu	Thr Leu Leu Gly Asn Gly			
	425	430			435
Ser Leu Ile Tyr	Gln Val Gln Val Val	Gly Thr Ser Ser Glu Val			
	440	445			450
Val Ala Met Thr	Leu Glu Thr Lys Pro	Gln Arg Arg Asp Gln Arg			
	455	460			465
Thr Val Leu Cys	His Met Ala Gly Leu	Gln Pro Gly Gly His Thr			
	470	475			480
Ala Val Gly Ile	Cys Pro Gly Leu Gly	Ala Arg Gly Ala His Met			
	485	490			495
Leu Leu Gln Asn	Glu Leu Phe Leu Asn	Val Gly Thr Lys Asp Phe			
	500	505			510
Pro Asp Gly Glu	Leu Arg Gly His Val	Ala Ala Leu Pro Tyr Cys			
	515	520			525
Gly His Ser Ala	Arg His Asp Thr Leu	Pro Val Pro Leu Ala Gly			
	530	535			540
Ala Leu Val Leu	Pro Pro Val Lys Ser	Gln Ala Ala Gly His Ala			
	545	550			555
Trp Leu Ser Leu	Asp Thr His Cys His	Leu His Tyr Glu Val Leu			
	560	565			570
Leu Ala Gly Leu	Gly Gly Ser Glu Gln	Gly Thr Val Thr Ala His			
	575	580			585
Leu Leu Gly Pro	Pro Gly Thr Pro Gly	Pro Arg Arg Leu Leu Lys			
	590	595			600
Gly Phe Tyr Gly	Ser Glu Ala Gln Gly	Val Val Lys Asp Leu Glu			
	605	610			615
Pro Glu Leu Leu	Arg His Leu Ala Lys	Gly Met Ala Ser Leu Met			
	620	625			630
Ile Thr Thr Lys	Gly Ser Pro Arg Gly	Glu Leu Arg Gly Gln Val			
	635	640			645
His Ile Ala Asn	Gln Cys Glu Val Gly	Gly Leu Arg Leu Glu Ala			
	650	655			660

Ala	Gly	Ala	Glu	Gly 665	Val	Arg	Ala	Leu	Gly 670	Ala	Pro	Asp	Thr	Ala 675
Ser	Ala	Ala	Pro	Pro 680	Val	Val	Pro	Gly	Leu 685	Pro	Ala	Leu	Ala	Pro 690
Ala	Lys	Pro	Gly	Gly 695	Pro	Gly	Arg	Pro	Arg 700	Asp	Pro	Asn	Thr	Cys 705
Phe	Phe	Glu	Gly	Gln 710	Gln	Arg	Pro	His	Gly 715	Ala	Arg	Trp	Ala	Pro 720
Asn	Tyr	Asp	Pro	Leu 725	Cys	Ser	Leu	Cys	Thr 730	Cys	Gln	Arg	Arg	Thr 735
Val	Ile	Cys	Asp	Pro 740	Val	Val	Cys	Pro	Pro 745	Pro	Ser	Cys	Pro	His 750
Pro	Val	Gln	Ala	Pro 755	Asp	Gln	Cys	Cys	Pro 760	Val	Cys	Pro	Glu	Lys 765
Gln	Asp	Val	Arg	Asp 770	Leu	Pro	Gly	Leu	Pro 775	Arg	Ser	Arg	Asp	Pro 780
Gly	Glu	Gly	Cys	Tyr 785	Phe	Asp	Gly	Asp	Arg 790	Ser	Trp	Arg	Ala	Ala 795
Gly	Thr	Arg	Trp	His 800	Pro	Val	Val	Pro	Pro 805	Phe	Gly	Leu	Ile	Lys 810
Cys	Ala	Val	Cys	Thr 815	Cys	Lys	Gly	Gly	Thr 820	Gly	Glu	Val	His	Cys 825
Glu	Lys	Val	Gln	Cys 830	Pro	Arg	Leu	Ala	Cys 835	Ala	Gln	Pro	Val	Arg 840
Val	Asn	Pro	Thr	Asp 845	Cys	Cys	Lys	Gln	Cys 850	Pro	Val	Gly	Ser	Gly 855
Ala	His	Pro	Gln	Leu 860	Gly	Asp	Pro	Met	Gln 865	Ala	Asp	Gly	Pro	Arg 870
Gly	Cys	Arg	Phe	Ala 875	Gly	Gln	Trp	Phe	Pro 880	Glu	Ser	Gln	Ser	Trp 885
His	Pro	Ser	Val	Pro 890	Pro	Phe	Gly	Glu	Met 895	Ser	Cys	Ile	Thr	Cys 900
Arg	Cys	Gly	Ala	Gly 905	Val	Pro	His	Cys	Glu 910	Arg	Asp	Asp	Cys	Ser 915
Leu	Pro	Leu	Ser	Cys 920	Gly	Ser	Gly	Lys	Glu 925	Ser	Arg	Cys	Cys	Ser 930
Arg	Cys	Thr	Ala	His 935	Arg	Arg	Pro	Pro	Glu 940	Thr	Arg	Thr	Asp	Pro 945
Glu	Leu	Glu	Lys	Glu	Ala	Glu	Gly	Ser						

<210> 8
 <211> 44
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic Oligonucleotide probe

 <400> 8
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 <210> 9
 <211> 28
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 9
 cggacgcgtg gggcctgcgc acccagct 28

 <210> 10
 <211> 36
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 10
 gccgctcccc gaacgggcag cggctccttc tcagaa 36

 <210> 11
 <211> 36
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 11
 ggcgcacagc acgcagcgca tcaccccgaa tggttc 36

 <210> 12
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic Oligonucleotide Probe

 <400> 12
 gtgctgcccc tccgttctga gaagga 26

 <210> 13

<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 13
gcagggtgct caaacaggac ac 22

<210> 14
<211> 3231
<212> DNA
<213> Homo Sapien

<400> 14
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tgcccgcgct ggccctgctg ctgctgctgc tcggagcggg gccccgaggc 200
agctccctgg ccaaccgggt gccgcgcgcg cccttgctctg cgcgccgggc 250
gtgcgccgcg cagccctgcc ggaatggggg tgtgtgcacc tcgcgccctg 300
agccggaccc gcagcacccg gccccgcgcg gcgagcctgg ctacagctgc 350
acctgccccg ccgggatctc cggcgccaac tgccagcttg ttgcagatcc 400
ttgtgccagc aacccttgtc accatggcaa ctgcagcagc agcagcagca 450
gcagcagcga tggctacctc tgcatttgca atgaaggcta tgaaggctcc 500
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cagggggact ggtcctcctg gaggagatgc tcgccttggg gaataatcac 950
tttattggtt ttgtgaatga ttctgtgact aagtctattg tggctttgcg 1000
cttaactctg gtggtgaagg tcagcacctg tgtgccgggg gagagtcacg 1050

caaatgactt ggagtgttca ggaaaaggaa aatgcaccac gaagccgtca 1100
 gaggcaactt tttcctgtac ctgtgaggag cagtacgtgg gtactttctg 1150
 tgaagaatac gatgcttgcc agaggaaacc ttgccaaaac aacgcgagct 1200
 gtattgatgc aaatgaaaag caagatggga gcaatttcac ctgtgtttgc 1250
 cttcctgggt atactggaga gctttgccag tccaagattg attactgcat 1300
 cctagacca tgcagaaatg gagcaacatg catttccagt ctcagtggat 1350
 tcacctgcca gtgtccagaa ggatacttcg gatctgcttg tgaagaaaag 1400
 gtggaccctt ggcctcgtc tccgtgccag aacaacggca cctgctatgt 1450
 ggacggggta cactttacct gcaactgcag cccgggcttc acagggccga 1500
 cctgtgcca gcttattgac ttctgtgccc tcagccctg tgctcatggc 1550
 acgtgccga gcgtgggcac cagctacaaa tgccctctgtg atccaggta 1600
 ccatggctc tactgtgagg aggaatataa tgagtgcctc tccgtccat 1650
 gcctgaatgc agccacctgc agggacctcg ttaatggcta tgagtgtgtg 1700
 tgccgtggcag aatacaaagg aacacactgt gaattgtaca aggatccctg 1750
 cgctaacgtc agctgtctga acggagccac ctgtgacagc gacggcctga 1800
 atggcacgtg catctgtgca cccgggttta cagggaaga gtgcgacatt 1850
 gacataaatg aatgtgacag taaccctcgc caccatggtg ggagctgcct 1900
 ggaccagccc aatgggtata actgccactg cccgcatggt tgggtgggag 1950
 caaactgtga gatccacctc caatggaagt ccgggcacat ggcggagagc 2000
 ctcaccaaca tgccacggca ctccctctac atcatcattg gagccctctg 2050
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 tacaactgcc gcagcatcga cagcgagtgc agcaatgcca ttgcatccat 2200
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 gcccatcgc ctatgaagat tacagtcctg atgacaaacc cttggtcaca 2300
 ctgattaaaa ctaaagattt gtaatctttt tttggattat ttttcaaaaa 2350
 gatgagatac tacactcatt taaatatttt taagaaaata aaaagcttaa 2400
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 ctaattttct gcagctttta gtttggaaaa aatattttta aaacaaaatt 2500

				110					115					120
Cys	Ile	Cys	Asn	Glu	Gly	Tyr	Glu	Gly	Pro	Asn	Cys	Glu	Gln	Ala
				125					130					135
Leu	Pro	Ser	Leu	Pro	Ala	Thr	Gly	Trp	Thr	Glu	Ser	Met	Ala	Pro
				140					145					150
Arg	Gln	Leu	Gln	Pro	Val	Pro	Ala	Thr	Gln	Glu	Pro	Asp	Lys	Ile
				155					160					165
Leu	Pro	Arg	Ser	Gln	Ala	Thr	Val	Thr	Leu	Pro	Thr	Trp	Gln	Pro
				170					175					180
Lys	Thr	Gly	Gln	Lys	Val	Val	Glu	Met	Lys	Trp	Asp	Gln	Val	Glu
				185					190					195
Val	Ile	Pro	Asp	Ile	Ala	Cys	Gly	Asn	Ala	Ser	Ser	Asn	Ser	Ser
				200					205					210
Ala	Gly	Gly	Arg	Leu	Val	Ser	Phe	Glu	Val	Pro	Gln	Asn	Thr	Ser
				215					220					225
Val	Lys	Ile	Arg	Gln	Asp	Ala	Thr	Ala	Ser	Leu	Ile	Leu	Leu	Trp
				230					235					240
Lys	Val	Thr	Ala	Thr	Gly	Phe	Gln	Gln	Cys	Ser	Leu	Ile	Asp	Gly
				245					250					255
Arg	Ser	Val	Thr	Pro	Leu	Gln	Ala	Ser	Gly	Gly	Leu	Val	Leu	Leu
				260					265					270
Glu	Glu	Met	Leu	Ala	Leu	Gly	Asn	Asn	His	Phe	Ile	Gly	Phe	Val
				275					280					285
Asn	Asp	Ser	Val	Thr	Lys	Ser	Ile	Val	Ala	Leu	Arg	Leu	Thr	Leu
				290					295					300
Val	Val	Lys	Val	Ser	Thr	Cys	Val	Pro	Gly	Glu	Ser	His	Ala	Asn
				305					310					315
Asp	Leu	Glu	Cys	Ser	Gly	Lys	Gly	Lys	Cys	Thr	Thr	Lys	Pro	Ser
				320					325					330
Glu	Ala	Thr	Phe	Ser	Cys	Thr	Cys	Glu	Glu	Gln	Tyr	Val	Gly	Thr
				335					340					345
Phe	Cys	Glu	Glu	Tyr	Asp	Ala	Cys	Gln	Arg	Lys	Pro	Cys	Gln	Asn
				350					355					360
Asn	Ala	Ser	Cys	Ile	Asp	Ala	Asn	Glu	Lys	Gln	Asp	Gly	Ser	Asn
				365					370					375
Phe	Thr	Cys	Val	Cys	Leu	Pro	Gly	Tyr	Thr	Gly	Glu	Leu	Cys	Gln
				380					385					390
Ser	Lys	Ile	Asp	Tyr	Cys	Ile	Leu	Asp	Pro	Cys	Arg	Asn	Gly	Ala
				395					400					405

Thr Cys Ile Ser	Ser Leu Ser Gly Phe	Thr Cys Gln Cys Pro Glu	410	415	420
Gly Tyr Phe Gly	Ser Ala Cys Glu Glu	Lys Val Asp Pro Cys Ala	425	430	435
Ser Ser Pro Cys	Gln Asn Asn Gly Thr	Cys Tyr Val Asp Gly Val	440	445	450
His Phe Thr Cys	Asn Cys Ser Pro Gly	Phe Thr Gly Pro Thr Cys	455	460	465
Ala Gln Leu Ile	Asp Phe Cys Ala Leu	Ser Pro Cys Ala His Gly	470	475	480
Thr Cys Arg Ser	Val Gly Thr Ser Tyr	Lys Cys Leu Cys Asp Pro	485	490	495
Gly Tyr His Gly	Leu Tyr Cys Glu Glu	Glu Tyr Asn Glu Cys Leu	500	505	510
Ser Ala Pro Cys	Leu Asn Ala Ala Thr	Cys Arg Asp Leu Val Asn	515	520	525
Gly Tyr Glu Cys	Val Cys Leu Ala Glu	Tyr Lys Gly Thr His Cys	530	535	540
Glu Leu Tyr Lys	Asp Pro Cys Ala Asn	Val Ser Cys Leu Asn Gly	545	550	555
Ala Thr Cys Asp	Ser Asp Gly Leu Asn	Gly Thr Cys Ile Cys Ala	560	565	570
Pro Gly Phe Thr	Gly Glu Glu Cys Asp	Ile Asp Ile Asn Glu Cys	575	580	585
Asp Ser Asn Pro	Cys His His Gly Gly	Ser Cys Leu Asp Gln Pro	590	595	600
Asn Gly Tyr Asn	Cys His Cys Pro His	Gly Trp Val Gly Ala Asn	605	610	615
Cys Glu Ile His	Leu Gln Trp Lys Ser	Gly His Met Ala Glu Ser	620	625	630
Leu Thr Asn Met	Pro Arg His Ser Leu	Tyr Ile Ile Ile Gly Ala	635	640	645
Leu Cys Val Ala	Phe Ile Leu Met Leu	Ile Ile Leu Ile Val Gly	650	655	660
Ile Cys Arg Ile	Ser Arg Ile Glu Tyr	Gln Gly Ser Ser Arg Pro	665	670	675
Ala Tyr Glu Glu	Phe Tyr Asn Cys Arg	Ser Ile Asp Ser Glu Phe	680	685	690
Ser Asn Ala Ile	Ala Ser Ile Arg His	Ala Arg Phe Gly Lys Lys			

695

700

705

Ser Arg Pro Ala Met Tyr Asp Val Ser Pro Ile Ala Tyr Glu Asp
 710 715 720

Tyr Ser Pro Asp Asp Lys Pro Leu Val Thr Leu Ile Lys Thr Lys
 725 730 735

Asp Leu

<210> 16

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 16

tgtaaaacga cggccagtta aatagacctg caattattaa tct 43

<210> 17

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 17

caggaaacag ctatgaccac ctgcacacct gcaaataccat t 41

<210> 18

<211> 508

<212> DNA

<213> Homo Sapien

<400> 18

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acgaaagtgt gacccccctt tcaggctttc aggggggactg gtctctcttg 100

aggagatgct cgccttgagg aataatcact ttattgggtt tgtgaatgat 150

tctgtgacta agtctattgt ggctttgcgc ttaactctgg tggatgaagg 200

cagcacctgt gtgccggggg agagtcacgc aaatgacttg gagggttcag 250

gaaaaggaaa atgcaccacg aagccgtcag aggcaacttt ttctgtacc 300

tgtgaggagc agtacgtggg tactttctgt gaagaatacg atgcttgcca 350

gaggaaacct tgccaaaaca acgcgagctg tattgatgca aatgaaaagc 400

aagatgggag caatttcacc tgtgtttgcc ttctgggtta tactggagag 450

ctttgccaac cgaactgaga ttggagcgaa cgacctacac cgaactgaga 500

taggggag 508

<210> 19
 <211> 508
 <212> DNA
 <213> Homo Sapien

<400> 19
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 acgaaagtgt gacccccctt tcaggctttc agggggactg gtctccttg 100
 aggagatgct cgccttgggg aataatcact ttattggttt tgtgaatgat 150
 tctgtgacta agtctattgt ggctttgagc ttaactctgg tggatgaagg 200
 cagcacctgt gtgcgggggg agagtcacgc aaatgacttg gagtggtcag 250
 gaaaaggaaa atgcaccacg aagccgtcag aggcaacttt ttctgtacc 300
 tgtgaggagc agtacgtggg tactttctgt gaagaatacg atgcttgcca 350
 gaggaaacct tgccaaaaca acgcgagctg tattgatgca aatgaaaagc 400
 aagatgggag caatttcacc tgtgtttgcc ttctgggtta tactggagag 450
 ctttgccaac cgaactgaga ttggagcgaa cgacctacac cgaactgaga 500
 taggggag 508

<210> 20
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Oligonucleotide Probe

<400> 20
 ctctggaagg tcacggccac agg 23

<210> 21
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 21
 ctgagttcgg ttggcaaagc tctc 24

<210> 22
 <211> 69
 <212> DNA
 <213> Artificial Sequence

<220>

General Population		Non-Hispanic Whites		Non-Hispanic Blacks		Hispanics	
Age	Sex	Age	Sex	Age	Sex	Age	Sex
18-24	Male	18-24	Male	18-24	Male	18-24	Male
25-34	Female	25-34	Female	25-34	Female	25-34	Female
35-44	Male	35-44	Male	35-44	Male	35-44	Male
45-54	Female	45-54	Female	45-54	Female	45-54	Female
55-64	Male	55-64	Male	55-64	Male	55-64	Male
65-74	Female	65-74	Female	65-74	Female	65-74	Female
75-84	Male	75-84	Male	75-84	Male	75-84	Male
85-94	Female	85-94	Female	85-94	Female	85-94	Female
95-104	Male	95-104	Male	95-104	Male	95-104	Male
105-114	Female	105-114	Female	105-114	Female	105-114	Female
115-124	Male	115-124	Male	115-124	Male	115-124	Male
125-134	Female	125-134	Female	125-134	Female	125-134	Female
135-144	Male	135-144	Male	135-144	Male	135-144	Male
145-154	Female	145-154	Female	145-154	Female	145-154	Female
155-164	Male	155-164	Male	155-164	Male	155-164	Male
165-174	Female	165-174	Female	165-174	Female	165-174	Female
175-184	Male	175-184	Male	175-184	Male	175-184	Male
185-194	Female	185-194	Female	185-194	Female	185-194	Female
195-204	Male	195-204	Male	195-204	Male	195-204	Male
205-214	Female	205-214	Female	205-214	Female	205-214	Female
215-224	Male	215-224	Male	215-224	Male	215-224	Male
225-234	Female	225-234	Female	225-234	Female	225-234	Female
235-244	Male	235-244	Male	235-244	Male	235-244	Male
245-254	Female	245-254	Female	245-254	Female	245-254	Female
255-264	Male	255-264	Male	255-264	Male	255-264	Male
265-274	Female	265-274	Female	265-274	Female	265-274	Female
275-284	Male	275-284	Male	275-284	Male	275-284	Male
285-294	Female	285-294	Female	285-294	Female	285-294	Female
295-304	Male	295-304	Male	295-304	Male	295-304	Male
305-314	Female	305-314	Female	305-314	Female	305-314	Female
315-324	Male	315-324	Male	315-324	Male	315-324	Male
325-334	Female	325-334	Female	325-334	Female	325-334	Female
335-344	Male	335-344	Male	335-344	Male	335-344	Male
345-354	Female	345-354	Female	345-354	Female	345-354	Female
355-364	Male	355-364	Male	355-364	Male	355-364	Male
365-374	Female	365-374	Female	365-374	Female	365-374	Female
375-384	Male	375-384	Male	375-384	Male	375-384	Male
385-394	Female	385-394	Female	385-394	Female	385-394	Female
395-404	Male	395-404	Male	395-404	Male	395-404	Male
405-414	Female	405-414	Female	405-414	Female	405-414	Female
415-424	Male	415-424	Male	415-424	Male	415-424	Male
425-434	Female	425-434	Female	425-434	Female	425-434	Female
435-444	Male	435-444	Male	435-444	Male	435-444	Male
445-454	Female	445-454	Female	445-454	Female	445-454	Female
455-464	Male	455-464	Male	455-464	Male	455-464	Male
465-474	Female	465-474	Female	465-474	Female	465-474	Female
475-484	Male						

cagtgctccc tcatagatgg acgaaagtgt gacccccctt tcaggcgaga 50

<210> 23

<211> 1520

<212> DNA

<213> Homo Sapien

<400> 23

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acaccacgcc agggcccccc agagccctca ccacgctggg cgccccaga 100

gcccacacca tgccgggcac ctacgctccc tcgaccacac tcagtagtcc 150

cagcaccag ggccctgcaag agcagggcacg ggccctgatg cgggacttcc 200

cgctcgtgga cggccacaac gacctgcccc tggctctaag gcaggtttac 250

cagaaagggc tacaggatgt taacctgcgc aatttcagct acggccagac 300

cagcctggac aggcttagag atggcctcgt gggcgcccag ttctggtcag 350

cctatgtgcc atgccagacc caggaccggg atgccctgcg cctcaccctg 400

gagcagattg acctcatacg ccgcatgtgt gcctcctatt ctgagctgga 450

gcttgtgacc tcggctaaag ctctgaacga cactcagaaa ttggcctgcc 500

tcacgggtgt agaggggtggc cactcgctgg acaatagcct ctccatctta 550

cgtaccttct acatgctggg agtgcgctac ctgacgctca cccacacctg 600

caacacaccc tgggcagaga gctccgctaa gggcgctccac tccttctaca 650

acaacatcag cgggctgact gactttgggtg agaaggtggt ggcagaaatg 700

aaccgctgg gcatgatggt agacttatcc catgtctcag atgctgtggc 750

acggcgggcc ctggaagtgt cacaggcacc tgtgatcttc tcccactcgg 800

ctgcccgggg tgtgtgcaac agtgctcgga atgttctctga tgacatctctg 850

cagcttctga agaagaacgg tggcgtcgtg atggtgtctt tgtccatggg 900

agtaatacag tgcaacccat cagccaatgt gtccactgtg gcagatcact 950

tgcaccacat caaggctgtc attggatcca agttcatcgg gattggtgga 1000

gattatgatg gggccggcaa attccctcag gggctggaag acgtgtccac 1050

ataccgggc ctgatatagg agttgctgag tcgtggctgg agtgaggaag 1100

agcttcaggg tgccttcgt ggaaacctgc tgcgggtcctt cagacaaqtg 1150

Parameter	Value	Unit
Initial concentration	1.0	g/L
Initial pH	7.0	
Temperature	25	°C
Time	0, 1, 2, 4, 8, 16, 32, 64, 128, 256, 512, 1024, 2048, 4096, 8192, 16384, 32768, 65536, 131072, 262144, 524288, 1048576, 2097152, 4194304, 8388608, 16777216, 33554432, 67108864, 134217728, 268435456, 536870912, 1073741824, 2147483648, 4294967296, 8589934592, 17179869184, 34359738368, 68719476736, 137438953472, 274877906944, 549755813888, 1099511627776, 2199023255552, 4398046511104, 8796093022208, 17592186044416, 35184372088832, 70368744177664, 140737488355328, 281474976710656, 562949953421312, 1125899906842624, 2251799813685248, 4503599627370496, 9007199254740992, 18014398509481984, 36028797018963968, 72057594037927936, 144115188075855872, 288230376151711744, 576460752303423488, 1152921504606846976, 2305843009213693952, 4611686018427387904, 9223372036854775808, 18446744073709551616, 36893488147419103232, 73786976294838206464, 147573952589676412928, 295147905179352825856, 590295810358705651712, 1180591620717411303424, 2361183241434822606848, 4722366482869645213696, 9444732965739290427392, 18889465931478580854784, 37778931862957161709568, 75557863725914323419136, 151115727451828646838272, 302231454903657293676544, 604462909807314587353088, 1208925819614629174706176, 2417851639229258349412352, 4835703278458516698824704, 9671406556917033397649408, 19342813113834066795298816, 38685626227668133590597632, 77371252455336267181195264, 154742504910672534362390528, 309485009821345068724781056, 618970019642690137449562112, 1237940039285380274899124224, 2475880078570760549798248448, 4951760157141521099596496896, 9903520314283042199192993792, 19807040628566084398385987584, 39614081257132168796771975168, 79228162514264337593543950336, 158456325028528675187087900672, 316912650057057350374175801344, 633825300114114700748351602688, 1267650600228229401496703205376, 2535301200456458802993406410752, 5070602400912917605986812821504, 10141204801825835211973625643008, 20282409603651670423947251286016, 40564819207303340847894502572032, 81129638414606681695789005144064, 162259276829213363391578010288128, 324518553658426726783156020576256, 649037107316853453566312041152512, 1298074214633706907132624082305024, 2596148429267413814265248164610048, 5192296858534827628530496329220096, 10384593717069655257060992658440192, 20769187434139310514121985316880384, 41538374868278621028243970633760768, 83076749736557242056487941267521536, 166153499473114484112975882535043072, 332306998946228968225951765070086144, 664613997892457936451903530140172288, 1329227995784915872903807060280344576, 2658455991569831745807614120560689152, 5316911983139663491615228241121378304, 10633823966279326983230456482242756608, 21267647932558653966460912964485513216, 42535295865117307932921825928971026432, 85070591730234615865843651857942052864, 170141183460469231731687303715884105728, 340282366920938463463374607431768211456, 680564733841876926926749214863536422912, 1361129467683753853853498429727072845824, 2722258935367507707706996859454145691648, 5444517870735015415413993718908291383296, 10889035741470030830827987437816582766592, 21778071482940061661655974875633165533184, 43556142965880123323311949751266331066368, 87112285931760246646623899502532662132736, 174224571863520493293247799005065324265472, 348449143727040986586495598010130648530944, 696898287454081973172991196020261297061888, 1393796574908163946345982392040522594123776, 2787593149816327892691964784081045188247552, 5575186299632655785383929568162090376495104, 11150372599265311570767859136324180752990208, 22300745198530623141535718272648361505980416, 44601490397061246283071436545296723011960832, 89202980794122492566142873090593446023921664, 178405961588244985132285746181186892047843328, 356811923176489970264571492362373784095686656, 713623846352979940529142984724747568191373312, 1427247692705959881058285969449495136382746624, 2854495385411919762116571938898990272765493248, 5708990770823839524233143877797980545530986496, 11417981541647679048466287755595961091061972992, 2283596308329	

<211> 433

<213> Homo Sapien

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65 70 75

Ala Gln Phe Trp Ser Ala Tyr Val Pro Cys Gln Thr Gln Asp Arg
80 85 90

Asp Ala Leu Arg Leu Thr Leu Glu Gln Ile Asp Leu Ile Arg Arg
95 100 105

Met Cys Ala Ser Tyr Ser Glu Leu Glu Leu Val Thr Ser Ala Lys
110 115 120

Ala Leu Asn Asp Thr Gln Lys Leu Ala Cys Leu Ile Gly Val Glu
125 130 135

Gly Gly His Ser Leu Asp Asn Ser Leu Ser Ile Leu Arg Thr Phe
140 145 150

Tyr Met Leu Gly Val Arg Tyr Leu Thr Leu Thr His Thr Cys Asn
155 160 165

Thr Pro Trp Ala Glu Ser Ser Ala Lys Gly Val His Ser Phe Tyr
170 175 180

Asn Asn Ile Ser Gly Leu Thr Asp Phe Gly Glu Lys Val Val Ala	185	190	195
Glu Met Asn Arg Leu Gly Met Met Val Asp Leu Ser His Val Ser	200	205	210
Asp Ala Val Ala Arg Arg Ala Leu Glu Val Ser Gln Ala Pro Val	215	220	225
Ile Phe Ser His Ser Ala Ala Arg Gly Val Cys Asn Ser Ala Arg	230	235	240
Asn Val Pro Asp Asp Ile Leu Gln Leu Leu Lys Lys Asn Gly Gly	245	250	255
Val Val Met Val Ser Leu Ser Met Gly Val Ile Gln Cys Asn Pro	260	265	270
Ser Ala Asn Val Ser Thr Val Ala Asp His Phe Asp His Ile Lys	275	280	285
Ala Val Ile Gly Ser Lys Phe Ile Gly Ile Gly Gly Asp Tyr Asp	290	295	300
Gly Ala Gly Lys Phe Pro Gln Gly Leu Glu Asp Val Ser Thr Tyr	305	310	315
Pro Val Leu Ile Glu Glu Leu Leu Ser Arg Gly Trp Ser Glu Glu	320	325	330
Glu Leu Gln Gly Val Leu Arg Gly Asn Leu Leu Arg Val Phe Arg	335	340	345
Gln Val Glu Lys Val Gln Glu Glu Asn Lys Trp Gln Ser Pro Leu	350	355	360
Glu Asp Lys Phe Pro Asp Glu Gln Leu Ser Ser Ser Cys His Ser	365	370	375
Asp Leu Ser Arg Leu Arg Gln Arg Gln Ser Leu Thr Ser Gly Gln	380	385	390
Glu Leu Thr Glu Ile Pro Ile His Trp Thr Ala Lys Leu Pro Ala	395	400	405
Lys Trp Ser Val Ser Glu Ser Ser Pro His Met Ala Pro Val Leu	410	415	420
Ala Val Val Ala Thr Phe Pro Val Leu Ile Leu Trp Leu	425	430	

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<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 25

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<210> 26

<211> 24

<212> DNA

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<220>

<223> Synthetic oligonucleotide probe

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<210> 27

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 27

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<210> 28

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 28

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<210> 29

<211> 1416

<212> DNA

<213> Homo Sapien

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gccctgatgc gggacttccc gctcgtggac ggccacaacg acctgcccct 200

ggctctaagg caggtttacc agaaagggt acaggatggt aacctgogca 250

atttcagcta cgccagacc agcctggaca ggcttagaga tggcctcgtg 300

ggcgcccagt tctggtcagc ctatgtgcca tgccagaccc aggaccggga 350

tgccctgcgc ctaccctgg agcagattga cctcatacgc cgcattgtgtg 400

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Tyr Gly Gln Thr Ser Leu Asp Arg Leu Arg Asp Gly Leu Val Gly	65		70		75
Ala Gln Phe Trp Ser Ala Tyr Val Pro Cys Gln Thr Gln Asp Arg	80		85		90
Asp Ala Leu Arg Leu Thr Leu Glu Gln Ile Asp Leu Ile Arg Arg	95		100		105
Met Cys Ala Ser Tyr Ser Glu Leu Glu Leu Val Thr Ser Ala Lys	110		115		120
Ala Leu Asn Asp Thr Gln Lys Leu Ala Cys Leu Ile Gly Val Glu	125		130		135
Gly Gly His Ser Leu Asp Asn Ser Leu Ser Ile Leu Arg Thr Phe	140		145		150
Tyr Met Leu Gly Val Arg Tyr Leu Thr Leu Thr His Thr Cys Asn	155		160		165
Thr Pro Trp Ala Glu Ser Ser Ala Lys Gly Val His Ser Phe Tyr	170		175		180
Asn Asn Ile Ser Gly Leu Thr Asp Phe Gly Glu Lys Val Val Ala	185		190		195
Glu Met Asn Arg Leu Gly Met Met Val Asp Leu Ser His Val Ser	200		205		210
Asp Ala Val Ala Arg Arg Ala Leu Glu Val Ser Gln Ala Pro Val	215		220		225
Ile Phe Ser His Ser Ala Ala Arg Gly Val Cys Asn Ser Ala Arg	230		235		240
Asn Val Pro Asp Asp Ile Leu Gln Leu Leu Lys Lys Asn Gly Gly	245		250		255
Val Val Met Val Ser Leu Ser Met Gly Val Ile Gln Cys Asn Pro	260		265		270
Ser Ala Asn Val Ser Thr Val Ala Asp His Phe Asp His Ile Lys	275		280		285
Ala Val Ile Gly Ser Lys Phe Ile Gly Ile Gly Gly Asp Tyr Asp	290		295		300
Gly Ala Gly Lys Phe Pro Gln Gly Leu Glu Asp Val Ser Thr Tyr	305		310		315
Pro Val Leu Ile Glu Glu Leu Leu Ser Arg Gly Trp Ser Glu Glu	320		325		330
Glu Leu Gln Gly Val Leu Arg Gly Asn Leu Leu Arg Val Phe Arg	335		340		345

Gln Val Glu Lys	Val Gln Glu Glu Asn	Lys Trp Gln Ser Pro Leu	
	350	355	360
Glu Asp Lys Phe	Pro Asp Glu Gln Leu	Ser Ser Ser Cys His Ser	
	365	370	375
Asp Leu Ser Arg	Leu Arg Gln Arg Gln	Ser Leu Thr Ser Gly Gln	
	380	385	390
Glu Leu Thr Glu	Ile Pro Ile His Trp	Thr Ala Lys Leu Pro Ala	
	395	400	405
Lys Trp Ser Val	Ser Glu Ser Ser Pro	His Pro Asp Lys Thr His	
	410	415	420
Thr Cys Pro Pro	Cys Pro Ala Pro Glu	Leu Leu Gly Gly Pro Ser	
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Val Phe Leu Phe	Pro Pro Lys Pro Lys	Asp Thr	
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 <213> Homo Sapien

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 atccgcgcgg cgccgcgcgc cgttgctgcc cctgctgctg ctgctctgcg 200
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 tgccacatcc ccaaggacct ggctctcttt acgccctatg agatctgggt 750
 ggaggccacc aaccgcctgg gctctgcccg ctccgatgta ctcacgctgg 800

Ser Val His Gly Asp	Pro Pro Gly Ala Thr	Ala Glu Gly Leu Tyr	65	70	75
Trp Thr Leu Asn Gly	Arg Arg Leu Pro Pro	Glu Leu Ser Arg Val	80	85	90
Leu Asn Ala Ser Thr	Leu Ala Leu Ala Leu	Ala Asn Leu Asn Gly	95	100	105
Ser Arg Gln Arg Ser	Gly Asp Asn Leu Val	Cys His Ala Arg Asp	110	115	120
Gly Ser Ile Leu Ala	Gly Ser Cys Leu Tyr	Val Gly Leu Pro Pro	125	130	135
Glu Lys Pro Val Asn	Ile Ser Cys Trp Ser	Lys Asn Met Lys Asp	140	145	150
Leu Thr Cys Arg Trp	Thr Pro Gly Ala His	Gly Glu Thr Phe Leu	155	160	165
His Thr Asn Tyr Ser	Leu Lys Tyr Lys Leu	Arg Trp Tyr Gly Gln	170	175	180
Asp Asn Thr Cys Glu	Glu Tyr His Thr Val	Gly Pro His Ser Cys	185	190	195
His Ile Pro Lys Asp	Leu Ala Leu Phe Thr	Pro Tyr Glu Ile Trp	200	205	210
Val Glu Ala Thr Asn	Arg Leu Gly Ser Ala	Arg Ser Asp Val Leu	215	220	225
Thr Leu Asp Ile Leu	Asp Val Val Thr Thr	Asp Pro Pro Pro Asp	230	235	240
Val His Val Ser Arg	Val Gly Gly Leu Glu	Asp Gln Leu Ser Val	245	250	255
Arg Trp Val Ser Pro	Pro Ala Leu Lys Asp	Phe Leu Phe Gln Ala	260	265	270
Lys Tyr Gln Ile Arg	Tyr Arg Val Glu Asp	Ser Val Asp Trp Lys	275	280	285
Val Val Asp Asp Val	Ser Asn Gln Thr Ser	Cys Arg Leu Ala Gly	290	295	300
Leu Lys Pro Gly Thr	Val Tyr Phe Val Gln	Val Arg Cys Asn Pro	305	310	315
Phe Gly Ile Tyr Gly	Ser Lys Lys Ala Gly	Ile Trp Ser Glu Trp	320	325	330
Ser His Pro Thr Ala	Ala Ser Thr Pro Arg	Ser Glu Arg Pro Gly	335	340	345
Pro Gly Gly Gly Ala	Cys Glu Pro Arg Gly	Gly Glu Pro Ser Ser			

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ctccctagag	tccttcgtga	agctttttat	tcctaagagg	agaaaatcag	200
tcaccggcga	aatcgtgctg	attacaggag	ctgggcacatg	aattggggaga	250
ctgactgcct	atgaatttgc	taaacttaaa	agcaagctgg	ttctctggga	300
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Geographical Area		Population		Area		Population		Area		Population		Area		Population		Area		Population		Area	
Country	Region	Year	Population	Year	Area	Year	Population	Year	Area	Year	Population	Year	Area	Year	Population	Year	Area	Year	Population	Year	Area
Algeria	Algeria	1990	10,000,000	1990	2,381,400	1990	10,000,000	1990	2,381,400	1990	10,000,000	1990	2,381,400	1990	10,000,000	1990	2,381,400	1990	10,000,000	1990	2,381,400
Algeria	Algeria	2000	12,000,000	2000	2,381,400	2000	12,000,000	2000	2,381,400	2000	12,000,000	2000	2,381,400	2000	12,000,000	2000	2,381,400	2000	12,000,000	2000	2,381,400
Algeria	Algeria	2010	14,000,000	2010	2,381,400	2010	14,000,000	2010	2,381,400	2010	14,000,000	2010	2,381,400	2010	14,000,000	2010	2,381,400	2010	14,000,000	2010	2,381,400
Algeria	Algeria	2020	16,000,000	2020	2,381,400	2020	16,000,000	2020	2,381,400	2020	16,000,000	2020	2,381,400	2020	16,000,000	2020	2,381,400	2020	16,000,000	2020	2,381,400
Algeria	Algeria	2030	18,000,000	2030	2,381,400	2030	18,000,000	2030	2,381,400	2030	18,000,000	2030	2,381,400	2030	18,000,000	2030	2,381,400	2030	18,000,000	2030	2,381,400
Algeria	Algeria	2040	20,000,000	2040	2,381,400	2040	20,000,000	2040	2,381,400	2040	20,000,000	2040	2,381,400	2040	20,000,000	2040	2,381,400	2040	20,000,000	2040	2,381,400
Algeria	Algeria	2050	22,000,000	2050	2,381,400	2050	22,000,000	2050	2,381,400	2050	22,000,000	2050	2,381,400	2050	22,000,000	2050	2,381,400	2050	22,000,000	2050	2,381,400
Algeria	Algeria	2060	24,000,000	2060	2,381,400	2060	24,000,000	2060	2,381,400	2060	24,000,000	2060	2,381,400	2060	24,000,000	2060	2,381,400	2060	24,000,000	2060	2,381,400
Algeria	Algeria	2070	26,000,000	2070	2,381,400	2070	26,000,000	2070	2,381,400	2070	26,000,000	2070	2,381,400	2070	26,000,000	2070	2,381,400	2070	26,000,000	2070	2,381,400
Algeria	Algeria	2080	28,000,000	2080	2,381,400	2080	28,000,000	2080	2,381,400	2080	28,000,000	2080	2,381,400	2080	28,000,000	2080	2,381,400	2080	28,000,000	2080	2,381,400
Algeria	Algeria	2090	30,000,000	2090	2,381,400	2090	30,000,000	2090	2,381,400	2090	30,000,000	2090	2,381,400	2090	30,000,000	2090	2,381,400	2090	30,000,000	2090	2,381,400
Algeria	Algeria	2100	32,000,000	2100	2,381,400	2100	32,000,000	2100	2,381,400	2100	32,000,000	2100	2,381,400	2100	32,000,000	2100	2,381,400	2100	32,000,000	2100	2,381,400
Algeria	Algeria	2110	34,000,000	2110	2,381,400	2110	34,000,000	2110	2,381,400	2110	34,000,000	2110	2,381,400	2110	34,000,000	2110	2,381,400	2110	34,000,000	2110	2,381,400
Algeria	Algeria	2120	36,000,000	2120	2,381,400	2120	36,000,000	2120	2,381,400	2120	36,000,000	2120									

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32

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Ile Lys Asn Pro	Ser Thr Ser Leu Gly	Pro Thr Leu Glu Pro	Glu		
	230		235		240
Glu Val Val Asn	Arg Leu Met His Gly	Ile Leu Thr Glu Gln	Lys		
	245		250		255
Met Ile Phe Ile	Pro Ser Ser Ile Ala	Phe Leu Thr Thr Leu	Glu		
	260		265		270
Arg Ile Leu Pro	Glu Arg Phe Leu Ala	Val Leu Lys Arg Lys	Ile		
	275		280		285
Ser Val Lys Phe	Asp Ala Val Ile Gly	Tyr Lys Met Lys Ala	Gln		
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<223> Synthetic oligonucleotide probe

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<210> 41

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<212> DNA

<213> Homo Sapien

[illegible]

<210> 42

Parameter	Value	Unit
Initial concentration	1.0	mol/L
Initial temperature	25	°C
Initial pH	7.0	
Initial ionic strength	0.1	M
Initial buffer concentration	0.05	M
Initial enzyme concentration	0.01	mol/L
Initial substrate concentration	0.01	mol/L
Initial product concentration	0.0	mol/L
Initial inhibitor concentration	0.0	mol/L
Initial cofactor concentration	0.0	mol/L
Initial metal ion concentration	0.0	mol/L
Initial cosolvent concentration	0.0	mol/L
Initial surfactant concentration	0.0	mol/L
Initial stabilizer concentration	0.0	mol/L
Initial preservative concentration	0.0	mol/L
Initial nutrient concentration	0.0	mol/L
Initial water activity	1.0	
Initial relative humidity	100	%
Initial oxygen concentration	0.21	atm
Initial carbon dioxide concentration	0.04	atm
Initial nitrogen concentration	0.79	atm
Initial total gas pressure	1.0	atm
Initial total solid concentration	0.0	mol/L
Initial total liquid concentration	0.0	mol/L
Initial total concentration	0.0	mol/L
Initial total mass	0.0	g
Initial total volume	0.0	L
Initial total energy	0.0	J
Initial total enthalpy	0.0	J
Initial total entropy	0.0	J/K
Initial total free energy	0.0	J
Initial total Gibbs free energy	0.0	J
Initial total Helmholtz free energy	0.0	J
Initial total internal energy	0.0	J
Initial total kinetic energy	0.0	J
Initial total potential energy	0.0	J
Initial total mechanical energy	0.0	J
Initial total electrical energy	0.0	J
Initial total magnetic energy	0.0	J
Initial total nuclear energy	0.0	J
Initial total chemical energy	0.0	J
Initial total biological energy	0.0	J
Initial total environmental energy	0.0	J
Initial total system energy	0.0	J
Initial total universe energy	0.0	J

<211> 24

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<210> 49

<211> 1876

<212> DNA

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His	Leu	Cys	Ser	Ala 170	Gly	Gln	Thr	Ala	Ile 175	Glu	Ala	Phe	Val	Cys 180
Ala	Tyr	Ser	Pro	Gly 185	Gly	Asn	Trp	Glu	Val 190	Asn	Gly	Lys	Thr	Ile 195
Ile	Pro	Tyr	Lys	Lys 200	Gly	Ala	Trp	Cys	Ser 205	Leu	Cys	Thr	Ala	Ser 210
Val	Ser	Gly	Cys	Phe 215	Lys	Ala	Trp	Asp	His 220	Ala	Gly	Gly	Leu	Cys 225
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Arg	Leu	Asn	Ile	Ser 245	Thr	Cys	His	Cys	His 250	Cys	Pro	Pro	Gly	Tyr 255
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Tyr	Gly	Gly	Ala	Gln 290	Cys	Ala	Thr	Lys	Val 295	His	Phe	Pro	Phe	His 300
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Leu	Ala	Phe	Tyr	Leu 350	Gly	Arg	Leu	Glu	Thr 355	Thr	Asn	Glu	Val	Thr 360
Asp	Ser	Asp	Phe	Glu 365	Thr	Arg	Asn	Phe	Trp 370	Ile	Gly	Leu	Thr	Tyr 375
Lys	Thr	Ala	Lys	Asp 380	Ser	Phe	Arg	Trp	Ala 385	Thr	Gly	Glu	His	Gln 390
Ala	Phe	Thr	Ser	Phe 395	Ala	Phe	Gly	Gln	Pro 400	Asp	Asn	His	Gly	Leu 405

Val Trp Leu Ser Ala Ala Met Gly Phe Gly Asn Cys Val Glu Leu
410 415 420

Gln Ala Ser Ala Ala Phe Asn Trp Asn Asp Gln Arg Cys Lys Thr
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<210> 53

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<210> 54

<211> 2331

<212> DNA

<213> Homo Sapien

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<400> 58
 agccgctcct tctccgggtc atcg 24

<210> 59
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<210> 60
 <211> 1413
 <212> DNA
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 aatctgttta cgaaagacgt gacagtgatc gagggagagg ttgcgaccat 200

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Phe	Thr	Lys	Asp	Val	Thr	Val	Ile	Glu	Gly	Glu	Val	Ala	Thr	Ile		50	55	60
Ser	Cys	Gln	Val	Asn	Lys	Ser	Asp	Asp	Ser	Val	Ile	Gln	Leu	Leu		65	70	75
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Lys	Asp	Ser	Arg	Phe	Gln	Leu	Leu	Asn	Phe	Ser	Ser	Ser	Glu	Leu		95	100	105
Lys	Val	Ser	Leu	Thr	Asn	Val	Ser	Ile	Ser	Asp	Glu	Gly	Arg	Tyr		110	115	120
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Lys	Asp	Thr	Ala	Val	Glu	Gly	Glu	Glu	Ile	Glu	Val	Asn	Cys	Thr		155	160	165
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Pro	Gln	Pro	Val	Met	Val	Thr	Trp	Val	Arg	Val	Asp	Asp	Glu	Met		275	280	285
Pro	Gln	His	Ala	Val	Leu	Ser	Gly	Pro	Asn	Leu	Phe	Ile	Asn	Asn		290	295	300
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<400> 65
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<210> 66
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<400> 66
atagctgtgt ctgcgtctgc tgcg 24

<210> 67
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Arg	Pro	Glu	Asp	Leu 185	Ala	Gly	Leu	Ala	Ala 190	Leu	Gln	Glu	Leu	Asp 195
Val	Ser	Asn	Leu	Ser 200	Leu	Gln	Ala	Leu	Pro 205	Gly	Asp	Leu	Ser	Gly 210
Leu	Phe	Pro	Arg	Leu 215	Arg	Leu	Leu	Ala	Ala 220	Ala	Arg	Asn	Pro	Phe 225
Asn	Cys	Val	Cys	Pro 230	Leu	Ser	Trp	Phe	Gly 235	Pro	Trp	Val	Arg	Glu 240
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Asp	Phe	Gly	Cys	Pro 275	Ala	Thr	Thr	Thr	Thr 280	Ala	Thr	Val	Pro	Thr 285
Thr	Arg	Pro	Val	Val 290	Arg	Glu	Pro	Thr	Ala 295	Leu	Ser	Ser	Ser	Leu 300
Ala	Pro	Thr	Trp	Leu 305	Ser	Pro	Thr	Ala	Pro 310	Ala	Thr	Glu	Ala	Pro 315
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Pro	Gln	Asp	Cys	Pro 335	Pro	Ser	Thr	Cys	Leu 340	Asn	Gly	Gly	Thr	Cys 345
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Phe	Thr	Gly	Leu	Tyr 365	Cys	Glu	Ser	Gln	Met 370	Gly	Gln	Gly	Thr	Arg 375
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<223> Synthetic oligonucleotide probe

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<210> 74

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 74

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<210> 75

<211> 1077

<212> DNA

<213> Homo Sapien

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Val	Pro	Ile	Asn	Ala	Thr	Ser	Lys	Asp	Asp	Ser	Asp	Val	Thr	Glu	125	130	135
Val	Met	Trp	Gln	Pro	Ala	Leu	Arg	Arg	Gly	Arg	Gly	Leu	Gln	Ala	140	145	150
Gln	Gly	Tyr	Gly	Val	Arg	Ile	Gln	Asp	Ala	Gly	Val	Tyr	Leu	Leu	155	160	165
Tyr	Ser	Gln	Val	Leu	Phe	Gln	Asp	Val	Thr	Phe	Thr	Met	Gly	Gln	170	175	180
Val	Val	Ser	Arg	Glu	Gly	Gln	Gly	Arg	Gln	Glu	Thr	Leu	Phe	Arg	185	190	195
Cys	Ile	Arg	Ser	Met	Pro	Ser	His	Pro	Asp	Arg	Ala	Tyr	Asn	Ser	200	205	210
Cys	Tyr	Ser	Ala	Gly	Val	Phe	His	Leu	His	Gln	Gly	Asp	Ile	Leu	215	220	225
Ser	Val	Ile	Ile	Pro	Arg	Ala	Arg	Ala	Lys	Leu	Asn	Leu	Ser	Pro	230	235	240
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125	130	135
Ala Pro Gly Glu Arg Cys Lys Ser His Tyr Ala Ala Phe Ser Val		
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Gly Arg Lys Lys Pro Met His Ser Asn His Tyr Tyr Gln Thr Val		
155	160	165
Ile Phe Asp Thr Glu Phe Val Asn Leu Tyr Asp His Phe Asn Met		
170	175	180
Phe Thr Gly Lys Phe Tyr Cys Tyr Val Pro Gly Leu Tyr Phe Phe		
185	190	195
Ser Leu Asn Val His Thr Trp Asn Gln Lys Glu Thr Tyr Leu His		
200	205	210
Ile Met Lys Asn Glu Glu Glu Val Val Ile Leu Phe Ala Gln Val		
215	220	225
Gly Asp Arg Ser Ile Met Gln Ser Gln Ser Leu Met Leu Glu Leu		
230	235	240
Arg Glu Gln Asp Gln Val Trp Val Arg Leu Tyr Lys Gly Glu Arg		
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 <212> DNA
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<220>
 <223> Synthetic oligonucleotide probe

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<210> 80
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<220>
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<400> 80
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<210> 81

<211> 45
<212> DNA
<213> Artificial Sequence

<220>
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<210> 82
<211> 2284
<212> DNA
<213> Homo Sapien

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Lys	Lys	Ser	Leu	Glu 35	Asp	Val	Val	Ile	Asp 40	Ile	Gln	Ser	Ser	Leu 45
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Ser	Asp	Gln	Glu	Ile 215	Ala	His	Leu	Leu	Pro 220	Glu	Asn	Val	Ser	Ala 225
Leu	Pro	Ala	Thr	Val 230	Ala	Val	Ala	Ser	Pro 235	His	Thr	Thr	Ser	Ala 240
Thr	Pro	Lys	Pro	Ala 245	Thr	Leu	Leu	Pro	Thr 250	Asn	Ala	Ser	Val	Thr 255
Pro	Ser	Gly	Thr	Ser 260	Gln	Pro	Gln	Leu	Ala 265	Thr	Thr	Ala	Pro	Pro 270
Val	Thr	Thr	Val	Thr 275	Ser	Gln	Pro	Pro	Thr 280	Thr	Leu	Ile	Ser	Thr 285
Val	Phe	Thr	Arg	Ala 290	Ala	Ala	Thr	Leu	Gln 295	Ala	Met	Ala	Thr	Thr 300
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 <213> Artificial Sequence

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<220>
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 agtgtaagtc aagctccc 18

<210> 89
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<210> 90
 <211> 957
 <212> DNA
 <213> Homo Sapien

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 gggagaggcc tgtcctcaaa gctccagtc ccaaaaggca aaaatgtgac 200
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 aggcgataac tctggaccga tgacaaagtt tattcagagt gctgctccaa 450
 aatccctgct cttcatggtg acctatgacg acggaagcac aagactgaat 500

Economic Indicators		Social Indicators		Environmental Indicators		Health Indicators		Education Indicators		Infrastructure Indicators	
Indicator	Value	Indicator	Value	Indicator	Value	Indicator	Value	Indicator	Value	Indicator	Value
GDP (USD)	1200000000000	Population (Millions)	100	Air Quality Index	75	Life Expectancy (Years)	75	Enrollment Rate (%)	95	Road Network (km)	10000
Unemployment Rate (%)	5.5	Urbanization Rate (%)	60	Water Quality Index	80	Infant Mortality Rate (per 1000)	10	Graduation Rate (%)	90	Power Generation (MW)	5000
Inflation Rate (%)	2.0	Gender Equality Index	70	Forest Cover (%)	25	Maternal Mortality Rate (per 1000)	5	Research and Development (%)	1.5	Telephony (per 100)	100
Trade Balance (USD)	50000000000	Human Development Index	0.75	Waste Recycling Rate (%)	15	Prevalence of HIV (%)	0.5	Patent Applications (per 1000)	0.5	Internet Usage (%)	50
Government Expenditure (%)	15.0	Corruption Perception Index	65	Renewable Energy Share (%)	10	Malaria Prevalence (%)	0.2	Startup Ecosystem Score	7.0	Mobile Phone Usage (%)	80
Foreign Direct Investment (USD)	20000000000	World Economic Forum Index	85	Carbon Footprint (kg per capita)	1500	Tuberculosis Incidence (per 1000)	0.1	Startup Funding (USD)	1000000000	Smartphone Usage (%)	70
Debt to GDP Ratio (%)	40.0	Global Competitiveness Index	70	Energy Efficiency Index	60	Polio Incidence (per 1000)	0.01	Startup Success Rate (%)	10.0	Cloud Adoption (%)	30
Consumer Confidence Index	100	World Economic Forum Index	85	Greenhouse Gas Emissions (kg per capita)	2000	Dysentery Incidence (per 1000)	0.05	Startup Valuation (USD)	500000000	Big Data Adoption (%)	20
Real Estate Market Index	120	World Economic Forum Index	85	Water Consumption (liters per capita)	150	Measles Incidence (per 1000)	0.02	Startup Exit Rate (%)	5.0	AI Adoption (%)	10
Stock Market Index	15000	World Economic Forum Index	85	Land Use Change (hectares)	50000	Scarlet Fever Incidence (per 1000)	0.01	Startup Funding Round	Series A	Blockchain Adoption (%)	5
Commodity Price Index	110	World Economic Forum Index	85	Soil Degradation (hectares)	100000	Cholera Incidence (per 1000)	0.005	Startup Funding Amount	1000000	Quantum Computing Adoption (%)	2
Real Estate Market Index	120	World Economic Forum Index	85	Deforestation Rate (%)	0.5	Polio Incidence (per 1000)	0.001	Startup Funding Duration	12 months	Autonomous Vehicle Adoption (%)	1
Stock Market Index	15000	World Economic Forum Index	85	Water Pollution Incidents	50	Scarlet Fever Incidence (per 1000)	0.005	Startup Funding Success Rate	20%	Space Exploration Adoption (%)	0.5
Commodity Price Index	110	World Economic Forum Index	85	Waste Management Score	70	Cholera Incidence (per 1000)	0.002	Startup Funding Exit Rate	15%	Artificial Intelligence Adoption (%)	0.1
Real Estate Market Index	120	World Economic Forum Index	85	Renewable Energy Investment (USD)	10000000000	Polio Incidence (per 1000)	0.0005	Startup Funding Valuation	1000000000	Blockchain Adoption (%)	0.05
Stock Market Index	15000	World Economic Forum Index	85	Carbon Footprint Reduction (%)	5	Scarlet Fever Incidence (per 1000)	0.0001	Startup Funding Success Rate	25%	Quantum Computing Adoption (%)	0.01
Commodity Price Index	110	World Economic Forum Index	85	Water Quality Improvement (%)	10	Cholera Incidence (per 1000)	0.00005	Startup Funding Exit Rate	30%	Autonomous Vehicle Adoption (%)	0.01
Real Estate Market Index	120	World Economic Forum Index	85	Land Use Change Reduction (%)	5	Polio Incidence (per 1000)	0.00001	Startup Funding Success Rate	35%	Space Exploration Adoption (%)	0.001
Stock Market Index	15000	World Economic Forum Index	85	Soil Degradation Reduction (%)	5	Scarlet Fever Incidence (per 1000)	0.000005	Startup Funding Success Rate	40%	Artificial Intelligence Adoption (%)	0.001
Commodity Price Index	110	World Economic Forum Index	85	Deforestation Rate Reduction (%)	5	Cholera Incidence (per 1000)	0.000001	Startup Funding Success Rate	45%	Blockchain Adoption (%)	0.0001
Real Estate Market Index	120	World Economic Forum Index	85	Water Pollution Incidents Reduction (%)	5	Polio Incidence (per 1000)	0.0000001	Startup Funding Success Rate	50%	Quantum Computing Adoption (%)	0.00001
Stock Market Index	15000	World Economic Forum Index	85	Waste Management Score Improvement (%)	5	Scarlet Fever Incidence (per 1000)	0.00000001	Startup Funding Success Rate	55%	Autonomous Vehicle Adoption (%)	0.000001
Commodity Price Index	110	World Economic Forum Index	85	Renewable Energy Investment Increase (%)	5	Cholera Incidence (per 1000)	0.000000001	Startup Funding Success Rate	60%	Space Exploration Adoption (%)	0.00000001
Real Estate Market Index	120	World Economic Forum Index	85	Carbon Footprint Reduction Increase (%)	5	Polio Incidence (per 1000)	0.0000000001	Startup Funding Success Rate	65%	Artificial Intelligence Adoption (%)	0.0000000001
Stock Market Index	15000	World Economic Forum Index	85	Water Quality Improvement Increase (%)	5	Scarlet Fever Incidence (per 1000)	0.00000000001	Startup Funding Success Rate	70%	Blockchain Adoption (%)	0.00000000001
Commodity Price Index	110	World Economic Forum Index	85	Land Use Change Reduction Increase (%)	5	Cholera Incidence (per 1000)	0.000000000001	Startup Funding Success Rate	75%	Quantum Computing Adoption (%)	0.000000000001
Real Estate Market Index	120	World Economic Forum Index	85	Soil Degradation Reduction Increase (%)	5	Polio Incidence (per 1000)	0.0000000000001	Startup Funding Success Rate	80%	Autonomous Vehicle Adoption (%)	0.0000000000001
Stock Market Index	15000	World Economic Forum Index	85	Deforestation Rate Reduction Increase (%)	5	Scarlet Fever Incidence (per 1000)	0.00000000000001	Startup Funding Success Rate	85%	Space Exploration Adoption (%)	0.00000000000001
Commodity Price Index	110	World Economic Forum Index	85	Water Pollution Incidents Reduction (%)	5	Cholera Incidence (per 1000)	0.00000000				

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Leu	Ile	Pro	Asp	Ala	Pro	Leu	Ser	Ser	Ala	Ala	Tyr	Ser	Ile	Arg	
				35					40					45	
Ser	Ile	Gly	Glu	Arg	Pro	Val	Leu	Lys	Ala	Pro	Val	Pro	Lys	Arg	
				50					55					60	
Gln	Lys	Cys	Asp	His	Trp	Thr	Pro	Cys	Pro	Ser	Asp	Thr	Tyr	Ala	
				65					70					75	
Tyr	Arg	Leu	Leu	Ser	Gly	Gly	Gly	Arg	Ser	Lys	Tyr	Ala	Lys	Ile	
				80					85					90	
Cys	Phe	Glu	Asp	Asn	Leu	Leu	Met	Gly	Glu	Gln	Leu	Gly	Asn	Val	
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Ala	Arg	Gly	Ile	Asn	Ile	Ala	Ile	Val	Asn	Tyr	Val	Thr	Gly	Asn	
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Val	Thr	Ala	Thr	Arg	Cys	Phe	Asp	Met	Tyr	Glu	Gly	Asp	Asn	Ser	
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Gly	Pro	Met	Thr	Lys	Phe	Ile	Gln	Ser	Ala	Ala	Pro	Lys	Ser	Leu	
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Leu	Phe	Met	Val	Thr	Tyr	Asp	Asp	Gly	Ser	Thr	Arg	Leu	Asn	Asn	
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 Asn Met Lys Phe Arg Ser Ser Trp Val Phe Ile Ala Ala Lys Gly
 185 190 195
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<210> 94

<211> 24

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 94

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<210> 95

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<213> Artificial Sequence

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<210> 117

<211> 48
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